

Substitute Sequence Listing

<110> Vermeij, Paul

<120> Lawsonia intracellularis 26 kD subunit vaccine

<130> I-2003.023 US

<140>

<141>

<150> PCT/EP2004/053342

<151> 2004-12-08

<160> 2

<170> PatentIn version 3.3

<210> 1

<211> 856

<212> DNA

<213> Lawsonia intracellularis

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<221> CDS

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Met Lys Lys Leu Leu Leu Leu Leu Ser Ile Leu	
1 5 10	
ttt cta acc cca agt att acc ttg gcg gaa ggt aat act ttc aat gat	160
Phe Leu Thr Pro Ser Ile Thr Leu Ala Glu Gly Asn Thr Phe Asn Asp	
15 20 25	
agt ttc aac aag gct aag cgc ata ctg caa gat gag gtg tat tac gac	208
Ser Phe Asn Lys Ala Lys Arg Ile Leu Gln Asp Glu Val Tyr Tyr Asp	
30 35 40	
cac caa gtt aca cta tac tgc gga tat gaa tat gat gac caa aaa agg	256
His Gln Val Thr Leu Tyr Cys Gly Tyr Glu Tyr Asp Asp Gln Lys Arg	
45 50 55	
ata tgt ctc cct gat gga ttt ata gca gag aaa cat caa aaa aga tca	304
Ile Cys Leu Pro Asp Gly Phe Ile Ala Glu Lys His Gln Lys Arg Ser	
60 65 70 75	
tat aaa att gag tgg gaa cat agt gtg cct gct gag aat ttt ggc aga	352
Tyr Lys Ile Glu Trp Glu His Ser Val Pro Ala Glu Asn Phe Gly Arg	
80 85 90	
gct ttt act gaa tgg cgc gaa ggt cat cct ctt tgt gta gat aat aaa	400
Ala Phe Thr Glu Trp Arg Glu Gly His Pro Leu Cys Val Asp Asn Lys	
95 100 105	
ggt aaa agt ttc aaa gga cga aaa tgt gca gaa aaa gta aat aaa aca	448
Gly Lys Ser Phe Lys Gly Arg Lys Cys Ala Glu Lys Val Asn Lys Thr	
110 115 120	

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tat	aga	tat	atg	cag	tct	gat	atg	tac	aat	ttg	ttt	cca	gca	gtc	ggg	496
Tyr	Arg	Tyr	Met	Gln	Ser	Asp	Met	Tyr	Asn	Leu	Phe	Pro	Ala	Val	Gly	
125						130					135					
tct	gtc	aat	gct	gcg	aga	agc	aat	aag	caa	tac	tca	gag	tta	ctt	gga	544
Ser	Val	Asn	Ala	Ala	Arg	Ser	Asn	Lys	Gln	Tyr	Ser	Glu	Leu	Leu	Gly	
140					145					150					155	
gtt	caa	tct	gct	ttt	gga	acg	tgt	gag	gca	aaa	ata	gat	ggg	aat	aga	592
Val	Gln	Ser	Ala	Phe	Gly	Thr	Cys	Glu	Ala	Lys	Ile	Asp	Gly	Asn	Arg	
				160					165					170		
ttc	gaa	cca	ccg	gat	aga	gct	aaa	ggg	caa	gta	gcc	cgt	gct	gct	ctt	640
Phe	Glu	Pro	Pro	Asp	Arg	Ala	Lys	Gly	Gln	Val	Ala	Arg	Ala	Ala	Leu	
			175					180					185			
tat	atg	gat	aaa	gag	tac	aag	gaa	tac	aat	cta	agt	cgt	cag	caa	aga	688
Tyr	Met	Asp	Lys	Glu	Tyr	Lys	Glu	Tyr	Asn	Leu	Ser	Arg	Gln	Gln	Arg	
		190					195					200				
aga	ctt	ttt	gag	gct	tgg	agt	aat	atg	tat	cca	gtc	gat	gaa	tgg	gag	736
Arg	Leu	Phe	Glu	Ala	Trp	Ser	Asn	Met	Tyr	Pro	Val	Asp	Glu	Trp	Glu	
	205					210					215					
tgt	aca	cga	gcc	aaa	cga	atc	gaa	tct	ata	cag	gga	aat	gaa	aat	att	784
Cys	Thr	Arg	Ala	Lys	Arg	Ile	Glu	Ser	Ile	Gln	Gly	Asn	Glu	Asn	Ile	
220					225					230					235	
ttt	gta	aaa	aat	atg	tgt	atc	gaa	aag	ggg	tta	tgg	taa	acaaacgagg			833
Phe	Val	Lys	Asn	Met	Cys	Ile	Glu	Lys	Gly	Leu	Trp					
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Lys Arg Ile Leu Gln Asp Glu Val Tyr Tyr Asp His Gln Val Thr Leu
 35 40 45

Tyr Cys Gly Tyr Glu Tyr Asp Asp Gln Lys Arg Ile Cys Leu Pro Asp
 50 55 60

Gly Phe Ile Ala Glu Lys His Gln Lys Arg Ser Tyr Lys Ile Glu Trp
 65 70 75 80

Glu His Ser Val Pro Ala Glu Asn Phe Gly Arg Ala Phe Thr Glu Trp
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85

90

95

Arg Glu Gly His Pro Leu Cys Val Asp Asn Lys Gly Lys Ser Phe Lys
100 105 110

Gly Arg Lys Cys Ala Glu Lys Val Asn Lys Thr Tyr Arg Tyr Met Gln
115 120 125

Ser Asp Met Tyr Asn Leu Phe Pro Ala Val Gly Ser Val Asn Ala Ala
130 135 140

Arg Ser Asn Lys Gln Tyr Ser Glu Leu Leu Gly Val Gln Ser Ala Phe
145 150 155 160

Gly Thr Cys Glu Ala Lys Ile Asp Gly Asn Arg Phe Glu Pro Pro Asp
165 170 175

Arg Ala Lys Gly Gln Val Ala Arg Ala Ala Leu Tyr Met Asp Lys Glu
180 185 190

Tyr Lys Glu Tyr Asn Leu Ser Arg Gln Gln Arg Arg Leu Phe Glu Ala
195 200 205

Trp Ser Asn Met Tyr Pro Val Asp Glu Trp Glu Cys Thr Arg Ala Lys
210 215 220

Arg Ile Glu Ser Ile Gln Gly Asn Glu Asn Ile Phe Val Lys Asn Met
225 230 235 240

Cys Ile Glu Lys Gly Leu Trp
245